



1/21

ESX ORF DNA Sequence (1 to 1116) -> 1-phase Translation
DNA sequence 1116 b.p. ATGGCTGCAACC ... agtcggaactga linear 371 Amino acids
MW: 41428 Dalton

1/1
ATG GCT GCA ACC TGT GAG ATT AGC AAC TAC TTC AGT GCG ATG TAC ACC CTG GAG GGC TCT GTT CCC
Met ala ala thr cys glu ile ser asn ile phe ser asn tyr phe ser ala met tyr ser glu asp ser thr leu ala ser val pro
91/31
CCT GCT GCC ACC TTT GGG GCC GAT GAC TTG GTA CTG ACC CTG AGC AAC CCC CAG ATG TCA TTG GAG GGT ACA GAG AAG GCC AGC TGG TTG
pro ala ala thr phe gly ala asp asp leu val leu thr leu ser asn pro gln met ser leu glu gly thr glu lys ala ser trp leu
181/61
GGG GAA CAG CCC CAG TTC TGG TCG AAG ACG CAG GTT CTG GAC TGG ATC AGC TAC CAA GTG GAG AAG AAC TAC GAC GCA AGC GCC ATT
gly glu gln pro gln phe trp ser lys thr gln val leu asp trp ile ser tyr gln val glu lys asn lys tyr asp ala ser ala ile
271/91
GAC TTC TCA CGA TGT GAC ATG GAT GGC GCC ACC CTC TGC AAT TGT GCC CTT GAG GAG CTG GTC TTT GGG CCT CTG GGG GAC CAA
asp phe ser arg cys asp met asp gly ala thr leu cys asn cys ala leu glu glu leu arg leu val phe gly pro leu gly asp gln
361/121
CTC CAT GCC CAG CTG CAA GAC CTC ACT TCC AGC TCT TCT GAT GAG CTC AGT TGG ATC ATT GAG CTG CTG GAG AAG GAT GGC ATG GCC TTC
lau his ala gln leu arg asp leu thr ser ser ser asp glu leu ser trp ile ile glu leu leu lys asp gly met ala phe
451/151
CAG GAG GCC CTA GAC CCA GGG CCC TTT GAC CAG GGC AGC CCC TTT GCC CAG GAG CTG CTG GAC GAC GGT CAG CAA GCC AGC CCC TAC CAC
gln glu ala leu asp pro gly pro phe asp gln gly ser pro phe ala gln glu leu leu asp asp gly gln gln ala ser pro tyr his
541/181
CCC GGC AGC TGT GGC GCA-GGA GCC CCC TCC CCT GGC AGC TCT GAC GTC TCC ACC GCA GGG ACT GGT GCT TCT CCG AGC TCC CAC TCC TCA
pro gly ser cys gly ala gly ala pro ser pro gly ser ser asp val ser thr ala gly thr gly ala ser arg ser ser his ser ser
631/211
GAC TCC GGT GGA AGT GAC GTG GAC CTG GAT CCC ACT GAT GGC AAG CTC TTC CCC AGC GAT GGT TTT CGT GAC TGC AAG AAG GGG GAT CCC
asp ser gly gly ser asp val asp leu asp pro thr asp gly lys leu phe pro ser asp gly phe arg asp cys lys lys gly asp pro

Fig. 1

811/271
 AGA GGC ACC CAC CTG TGG GAG TTC ATC CCG GAC ATC CTC ATC CAC CCG GAG CTC AAC GAG GGC CTC ATG AAG TGG GAG AAT CGG CAT GAA
 arg gly thr his leu trp glu phe ile arg asp ile leu ile his pro glu leu asn glu gly leu met lys trp glu asn arg his glu
 901/301
 66C GTC TTC aag TTC CTG CGC TCC GAG GCT GTG GCC CAA CTA TGG GGC CAA AAG AAA AAG AAC AGC AAC ATG ACC TAC GAG AAG CTG AGC
 gly val phe lys phe leu arg ser glu ala val ala gln leu trp gly gln lys lys asn ser asn met thr tyr glu lys leu ser
 991/331
 CGG GCC ATG AGG TAC TAC AAA CGG GAG ATC CTG GAA CGG GTG GAT GGC CGG CGA CTC GTC TAC AAG TTT GGC AAA AAC TCA AGC GGC
 arg ala met arg tyr tyr lys arg glu ile leu glu arg val asp gly arg arg leu val tyr lys phe gly lys asn ser ser gly
 1081/361
 TGG AAG GAG GAA GAG GTT CTC CAG AGT CGG AAC TGA
 trp lys glu glu glu val leu gln ser arg asn OPA

Fig. 1 (cont.)

MAATCEISNIFSNYFSAMYSSSEDSTLASVPPAATFGADDLVLTLSNPQMSLEG 53
 TEKASNLGEQPQFWSKTQVLDNISYQVEKNKYDASAIDFSRCDMDGATLCNCA 106
 LEEELRVFGPLGDLHAQLRDLTSSSSDELSWIIELLEKDGMAFQEAALDPGPF 159
 DQGSFPAQELLDDGQQAAPYHPGSCGAGAPSPGSSDVSTAGTGASRSSHSSDS 212
GGSDVDLDPTDGKLFPSDGFRCCKGDPKHGKRKRGRPRKLSKEYWDCLEGKK 265
 SKHAPRGTHLWEFIRDILIHPELNEGLMKWENRHEGVFKELRSEAVAQLWGQK 318
KKNSNMITYEKLGRAMRYYYKREILERVDGRRLLVYKFGKNSSSGWKKEEVLQSRN 371

Fig. 2A

3/21

Consensus+: P W V W E G LC
 ESX (64-103): PQFWSKTQVLDWISYQVEKNKYDASAI~~DFSRCDMDGATLC~~
 P+ W++T V DW+ + V N++ +DF + M+GA LC
 ETS-1 (69-106: PRQWTE~~THVRDWMWAV~~--NEFSLKGVD~~FQKFCMNGAALC~~

Fig. 2B

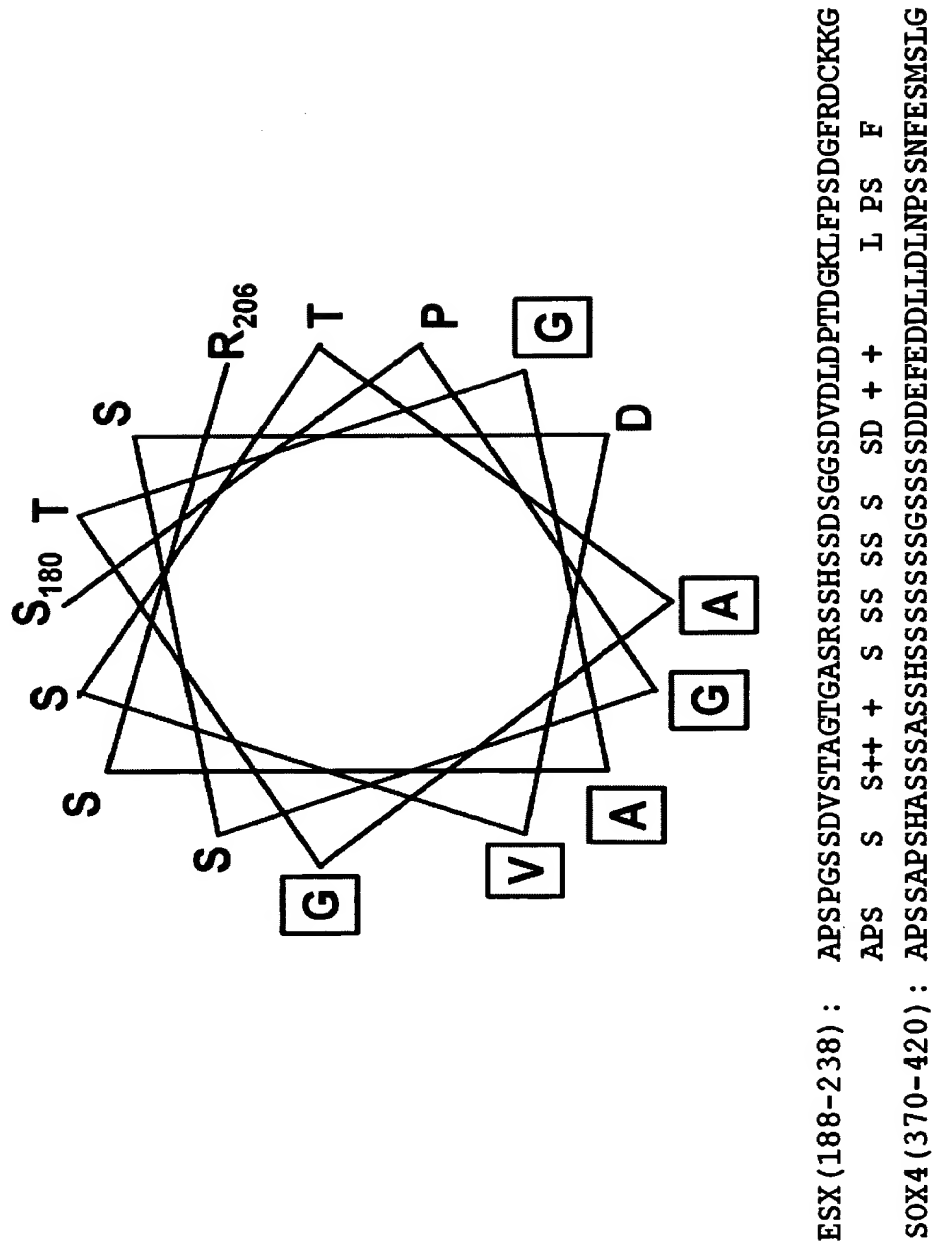


Fig. 2C

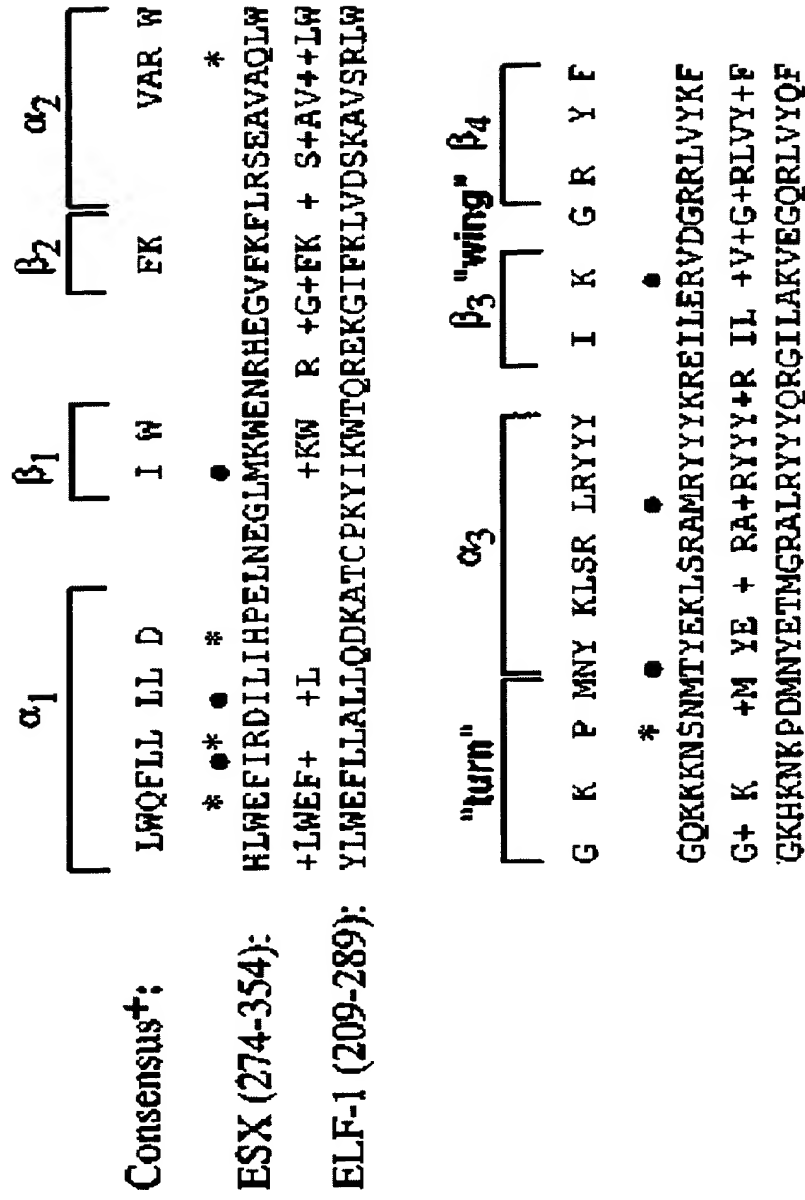


Fig. 2D

Human ESX Protein Sequence

MAATCEISNIFSNYFSAMYSSDSTLASVPPAATFGADDLVLTLSNPQMSLEG 53
TEKASWLGEQPQFWSKTQVLDWISYQVEKNKYDASAI DFSRCDMDGATLCNCA 106
LEELRLVFGPLGDQLHAQLRDLTSSSSDEL SWIIELLEKDGMAFQEA LDPGPF 159
DQGSPPFAQE LDDGQQASPYHPGSCGAGAPSPGSSDVSTAGTGASRSSHSSDS 212
GGSDVDLDPTDGKLFPSDGF RDCKKGD PKHGKRRGRPRKLSKEYWDCLEGKK 265
SKHAPRGTHLWEFIRDILIHPELNEGIMKWNRRHEGVFKFLRSEAVAQLWGQK 318
KKNSNMTYEKLSRAMRYYYKREILERVDGRRLVYKFGKNSSGWKEEVLQSRN 371

Fig. 2E

7/21

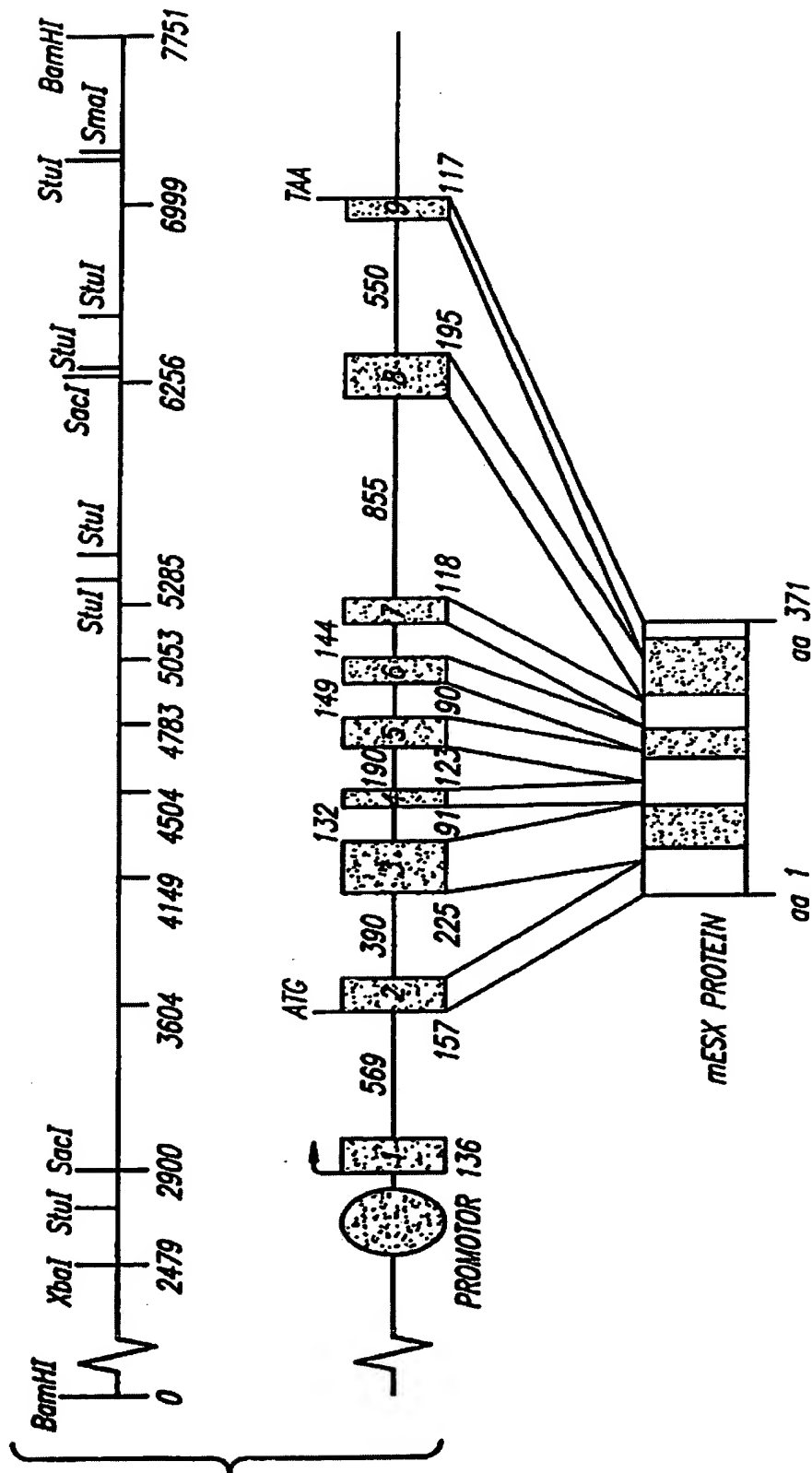


Fig. 3

1/1 31/11
 ATG GCT GCA ACC TGT GAG ATT AGC AAC ATT TTT AGC AAC TAC TTC AGT GCG ATG TAC AGC
 Met ala ala thr cys glu ile ser asn ile phe ser asn tyr phe ser ala met tyr ser
 61/21 91/31
 TCG GAG GAC TCC ACC CTG GCC TCT GTT CCC CCT GCT GCC ACC TTT GGG GCC GAT GAC TTG
 ser glu asp ser thr leu ala ser val pro pro ala ala thr phe gly ala asp asp leu
 121/41 151/51 E2 E3
 GTA CTG ACC CTG AGC AAC CCC CAG ATG TCA TTG GAG GGT ACA GAG AAC GCC AGC TGG TTG
 val leu thr leu ser asn pro gln met ser leu glu thr gly thr lys ala ser trp leu
 181/61 211/71
 GGG GAA CAG CCC CAG TTC TGG TCG AAG ACG CAG GTT CTG GAC TGG ATC AGC TAC CAA GTG
 gly glu gln pro gln phe thr trp ser lys thr gln val leu asp trp ile ser tyr gln val
 241/81 271/91
 GAG AAG AAC AAG TAC GAC GCA AGC GCC ATT GAC TTC TCA CGA TGT GAC ATG GAT GGC GCC
 glu lys asn lys tyr asp ala ser ala ile asp phe ser arg cys asp met asp gly ala
 301/101 331/111
 ACC CTC TGC AAT TGT GCC CTT GAG GAG CTG CGT CTG GTC TTT GGG CCT CTG GGG GAC CAA
 thr leu cys asn cys ala leu glu glu leu arg leu val phe gly pro leu gly asp gln
 361/121 E3 E4 391/131
 CTC CAT GCC CAG CTG CGA GAC CTC ACT TCC AGC TCT TCT GAT GAG CTC AGT TGG ATC ATT
 leu his ala gln leu arg asp leu thr ser ser ser asp glu leu ser trp ile ile
 421/141 451/151 E4 E5
 GAG CTG CTG GAG AAG GAT GGC ATG GCC TTC CAG GAG GCC CTA GAC CCA GGG CCC TTT GAC
 glu leu leu glu lys asp gly met ala phe gln glu ala leu asp pro gly pro phe asp

Fig. 4

481/161 511/171
 CAG GGC AGC CCC TTT GCC CAG GAG CTG CTG GAC GAC GGT CAG CAA GCC AGC CCC TAC CAC
 gln gly ser pro phe ala gln glu leu leu asp asp gly gln ala ser pro tyr his
 541/181 571/191 E5 E6
 CCC GGC AGC TGT GGC GCA GGA GCC Ccc TCC CCT GGC AGC TCT GAC GTC TCC ACC GCA GGG
 pro gly ser cys gly ala gly ala pro ser pro gly ser ser asp val ser thr ala gly
 601/201 631/211
 ACT GGT GCT TCT CGG AGC TCC CAC TCC TCA GAC TCC GGT GGA AGT GAC GTG GAC CTG GAT
 thr gly ala ser arg ser ser his ser ser asp ser gly gly ser asp val asp leu asp
 661/221 E6 E7 E8 E9
 CCC ACT GAT GGC AAG CTC TTC CCC AGC GAT GGT TTT CGT GAC TGC AAG AAG GGG GAT CCC
 pro thr asp gly lys leu phe pro ser asp gly phe arg asp cys lys lys gly asp pro
 721/241 751/251
 AAG CAC GGC AAG CGG AAA CGA GGC CGG CCC CGA AAG CTG AGC AAA GAG TAC TGG GAC TGT
 lys his gly lys arg lys arg gly arg pro arg lys leu ser lys glu tyr trp asp cys
 781/261 E7 E8
 CTC GAG GGC AAG AAG AGC AAG CAC GCG CCC AGA GGC ACC CAC CTG TGG GAG TTC ATC CGG
 leu glu gly lys ser lys his ala pro arg gly thr his leu trp glu phe ile arg
 841/281 871/291
 GAC ATC CTC ATC CAC CCG GAG CTC AAC GAG GGC CTC ATG AAG TGG GAG AAT CGG CAT GAA
 asp ile leu ile his pro glu leu asn glu gly leu met lys trp glu asn arg his glu
 901/301 931/311
 GGC GTC TTC aag TTC CTG CGC TCC GAG GCT GTG GCC CAA CTA TGG GGC CAA AAG AAA AAG
 gly val phe lys phe leu arg ser glu ala val ala gln leu trp gly gln lys lys lys

Fig. 4 (cont.)

10/21

961/321
AAC AGC AAC ATG ACC TAC GAG AAG CTG AGC CGG GCC ATG AGG TAC TAC AAA CGG GAG
asn ser asn met thr tyr glü lys leu ser arg ala met arg tyr tyr lys arg glü
1021/341
ATC CTG GAA CGG GTG GAT GGC CGG CGA CTC GTC TAC AAG TTT GGC AAA AAC TCA AGC GGC
ile leu glü arg val asp gly arg arg leu val tyr lys phe gly lys asn ser ser gly
1081/361
TGG AAG GAG GAA GAG GTT CTC CAG AGT CGG AAC TGA
trp lys glü glü glü val leu ser arg asn OPA

991/331 E8 E9

Fig. 4 (cont.)

11/21

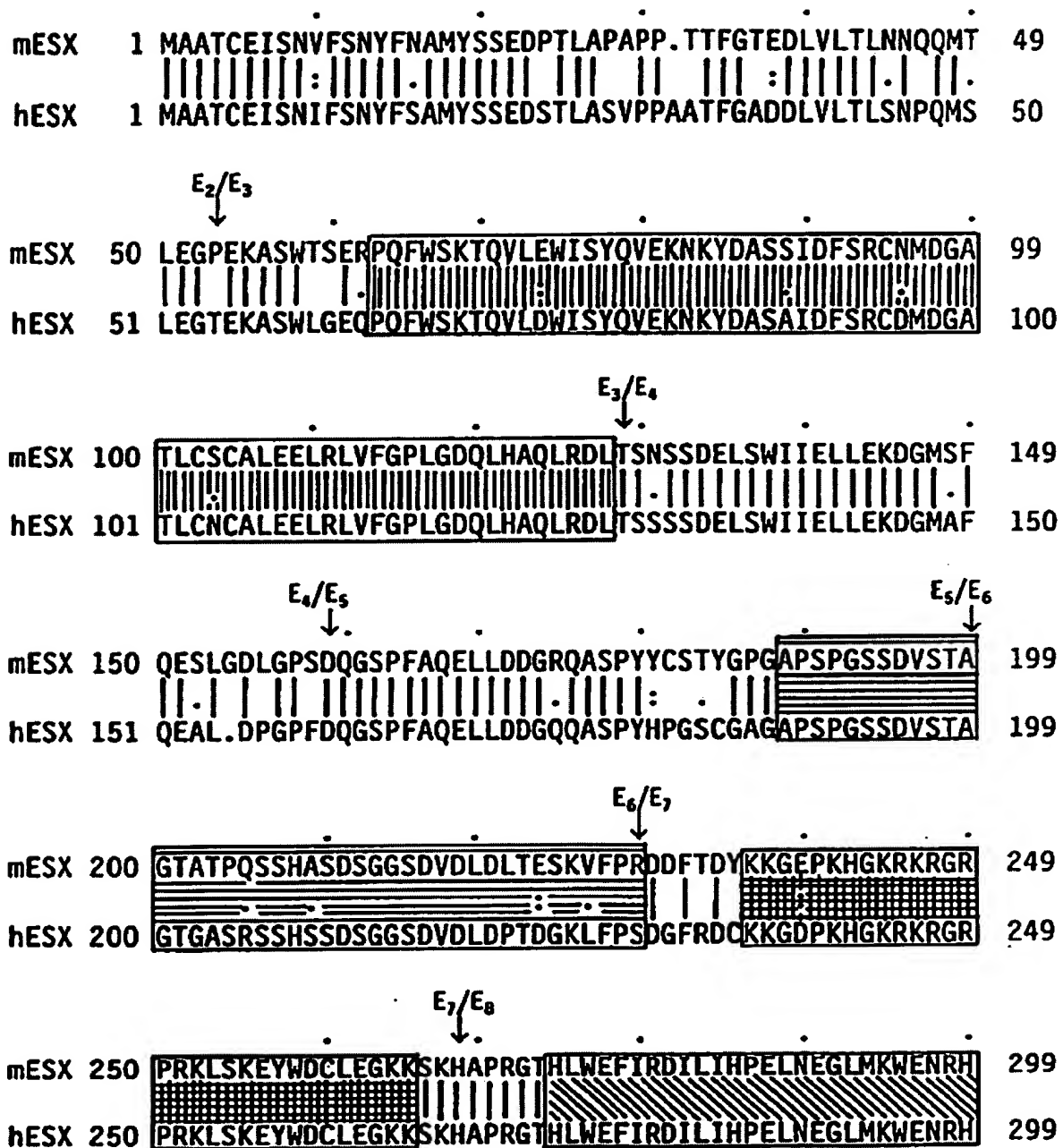


Fig. 5

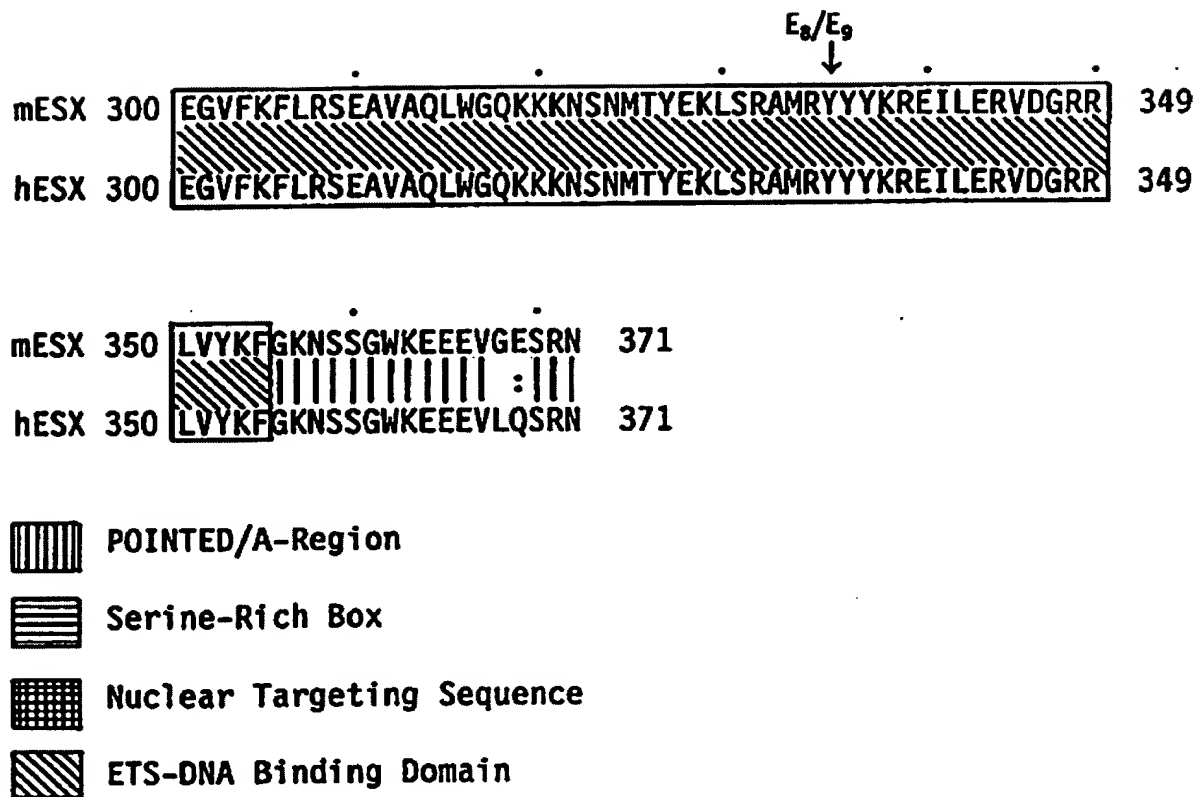


Fig. 5 (cont.)

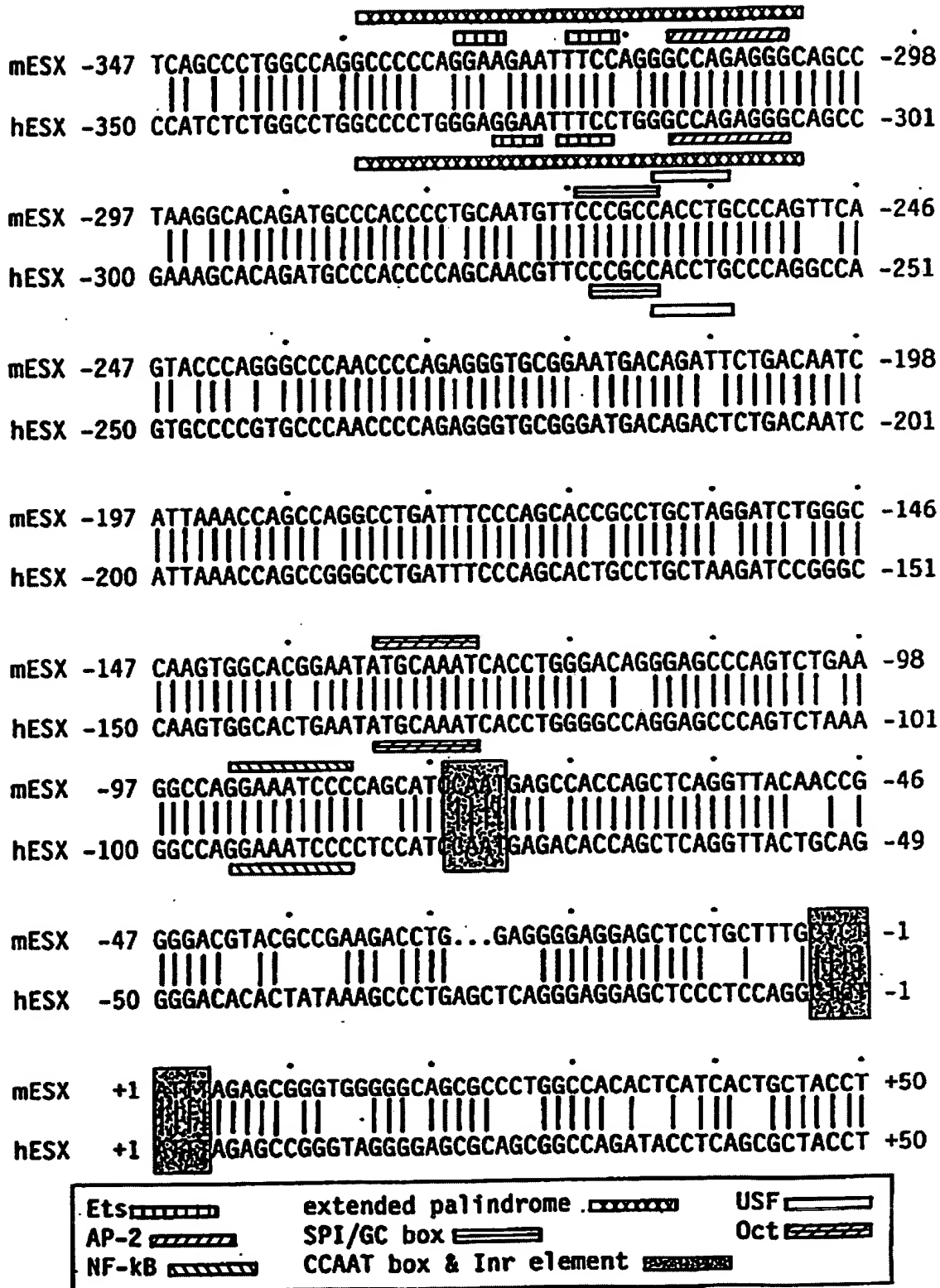


Fig. 6

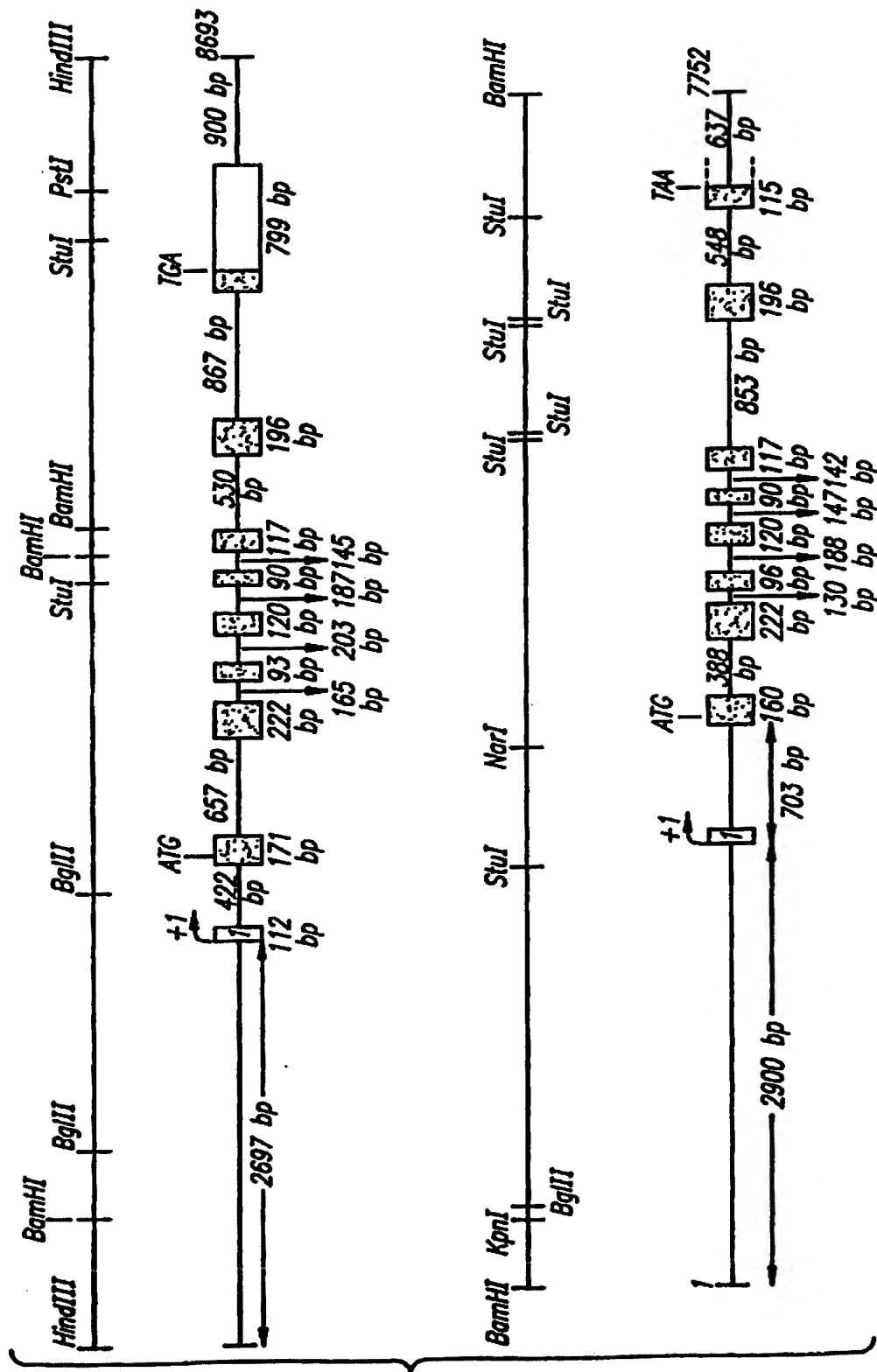
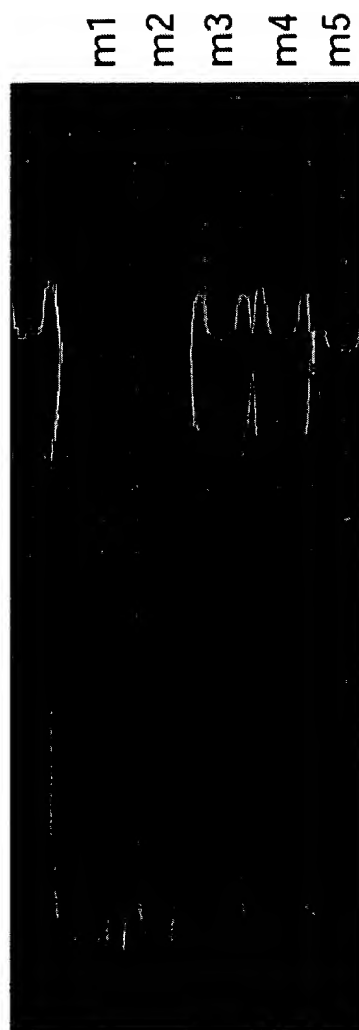


Fig. 7

15/21



WT 5' GGAGGAGGGCTGCTTGAGGAAGTATAAGAAT 3'
m1 5' -----TA----- 3'
m2 5' -----C----- 3'
m3 5' -----AG----- 3'
m4 5' -----CC----- 3'
m5 5' -----C----- 3'

Fig. 8A

16/21

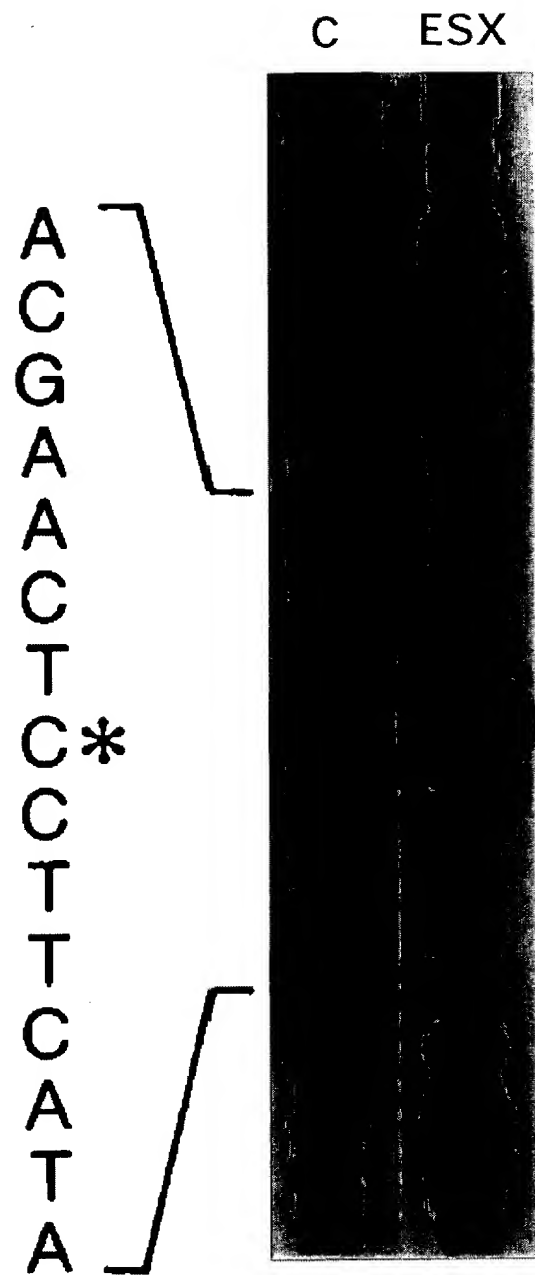


Fig. 8B

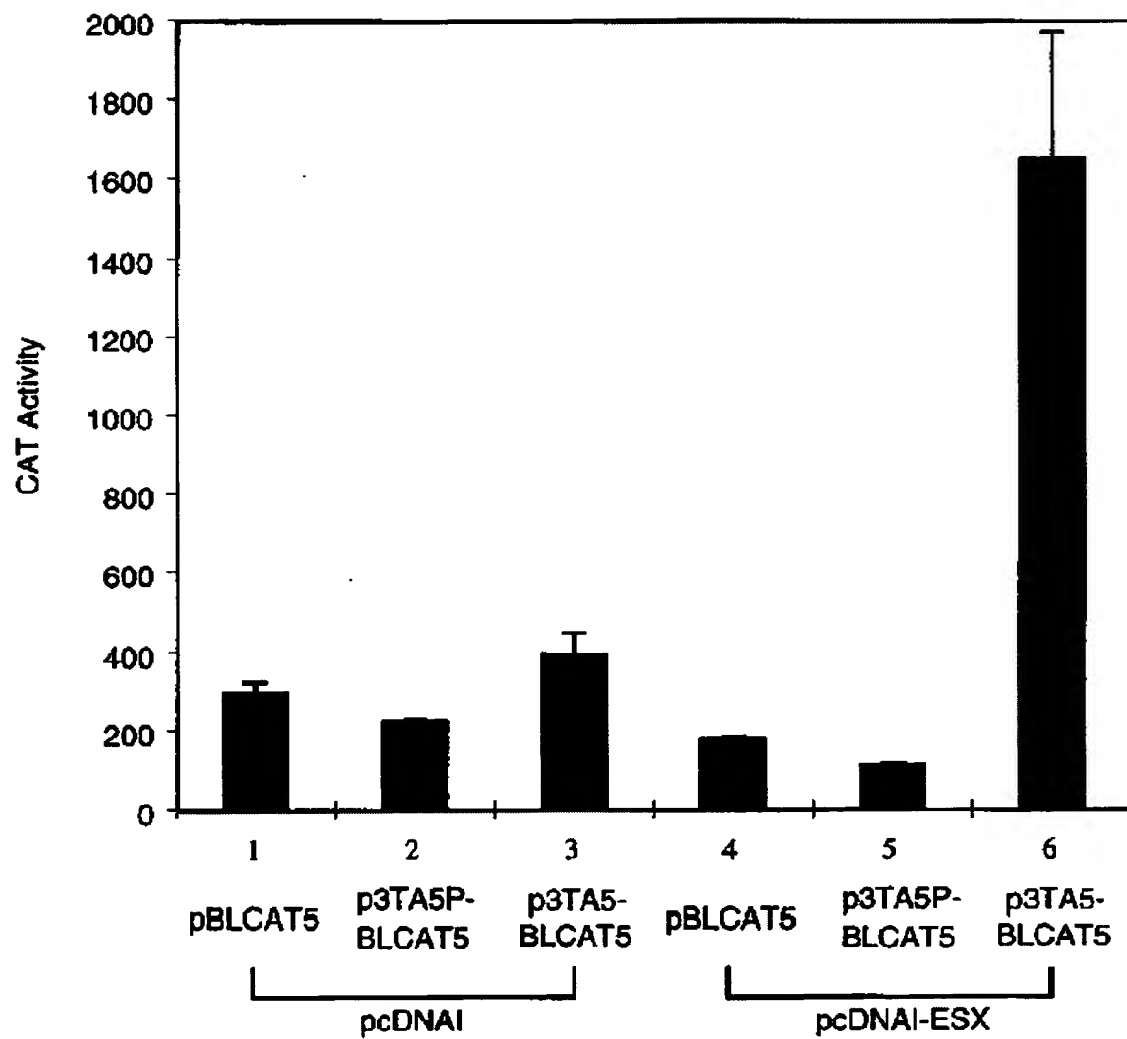


Fig. 8C

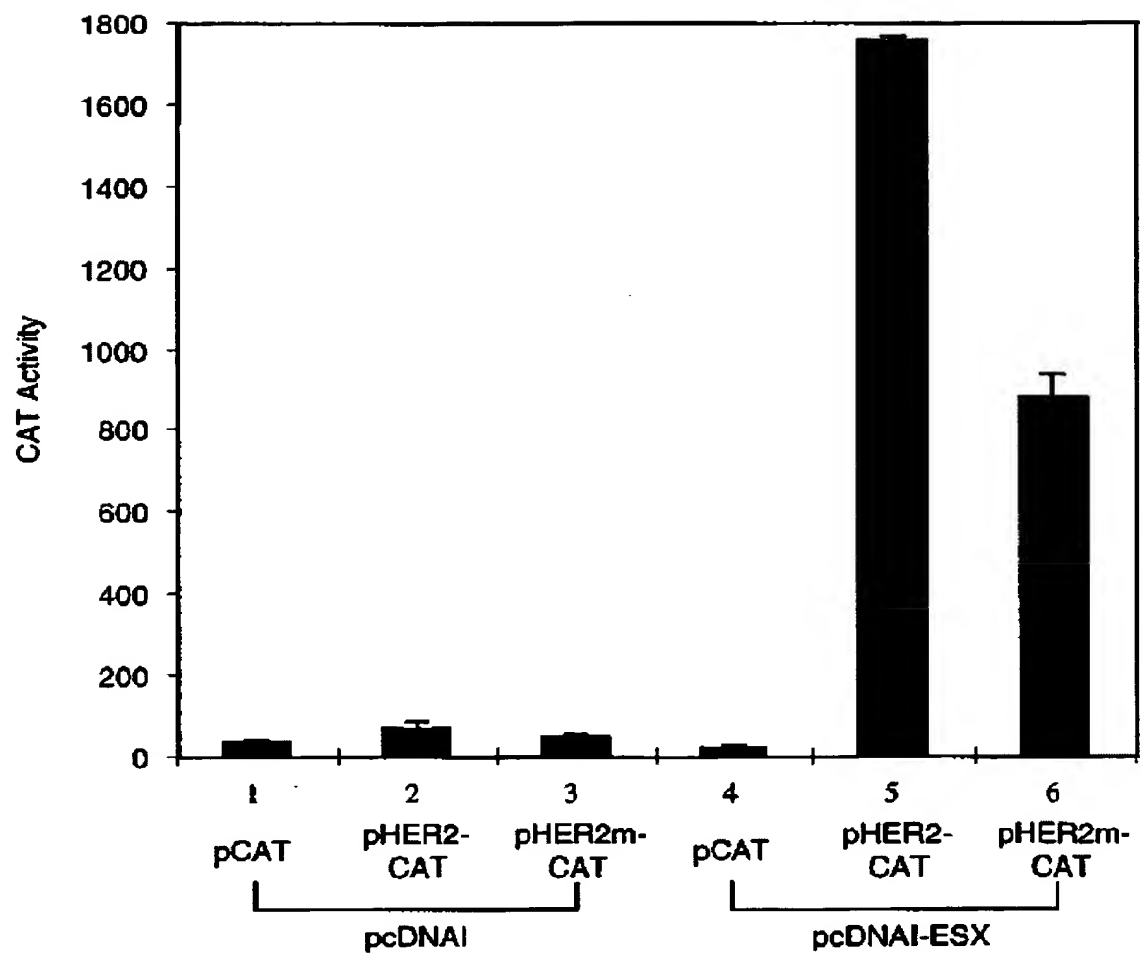


Fig. 8D

19/21

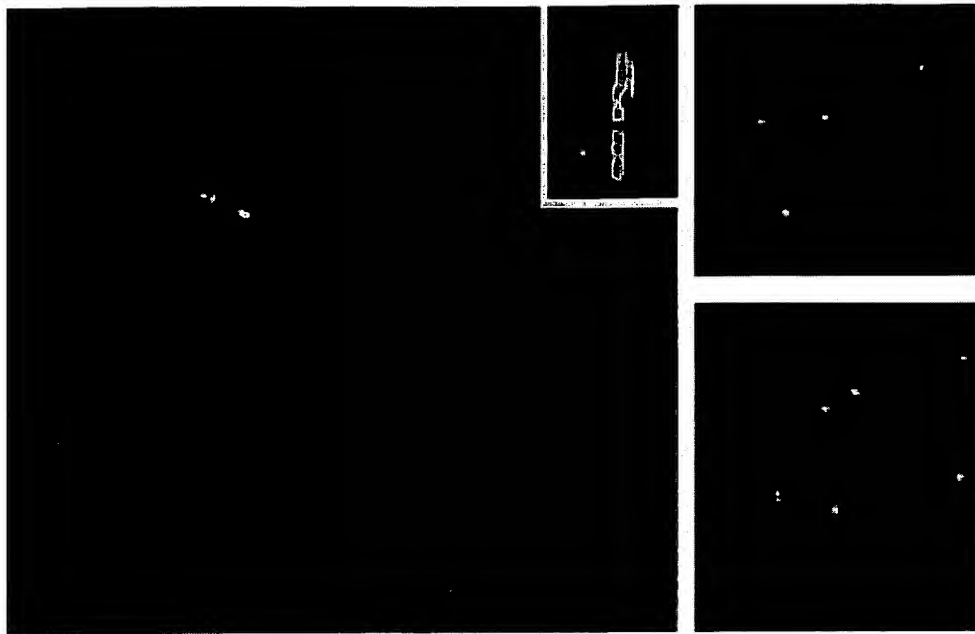


Fig. 8E

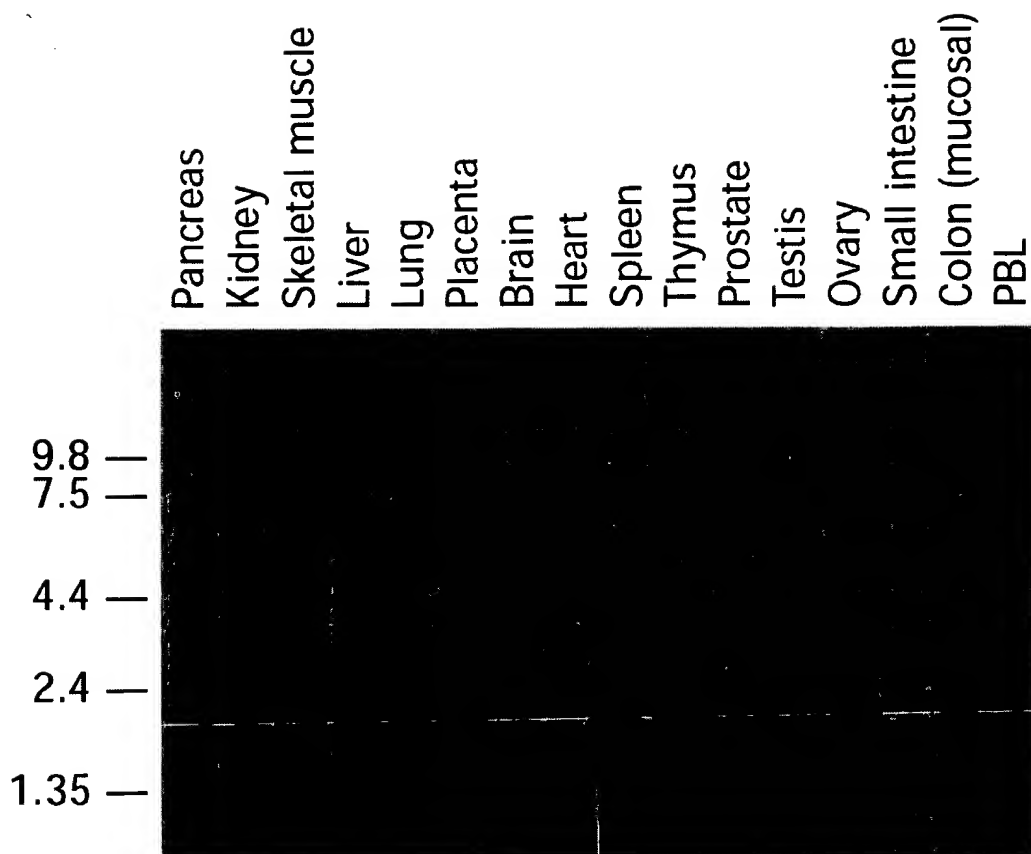


Fig. 9A

20/21

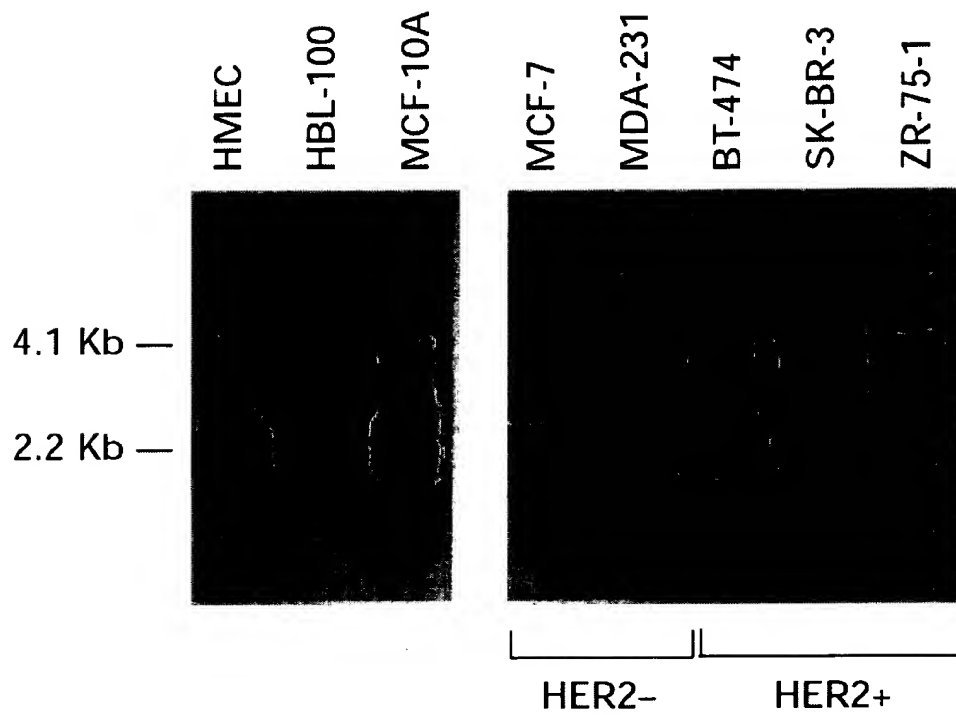


Fig. 9B

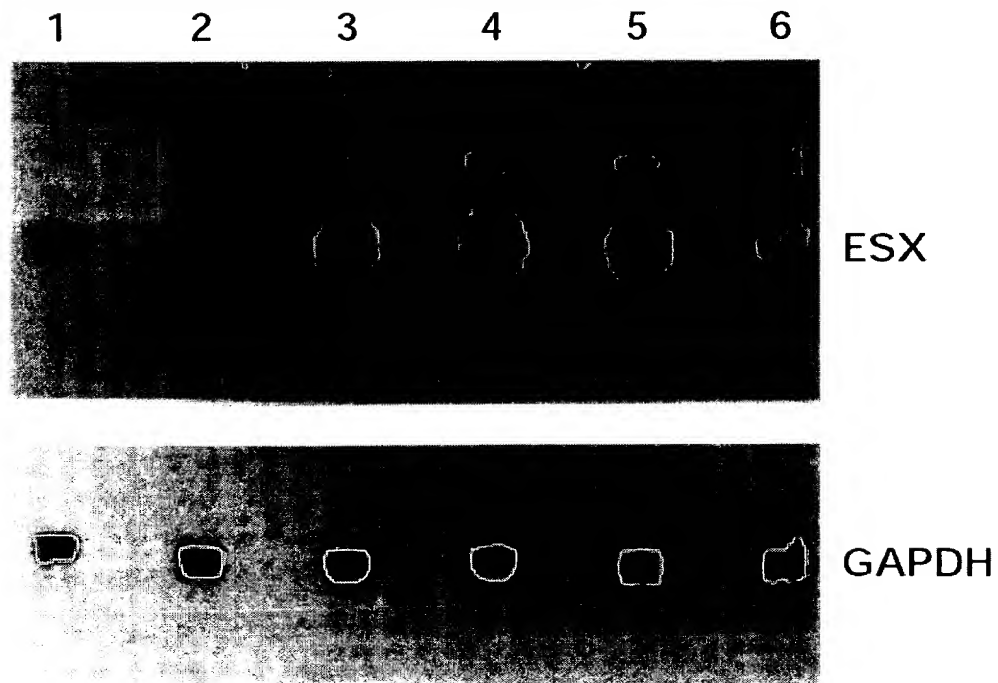


Fig. 9C

21/21

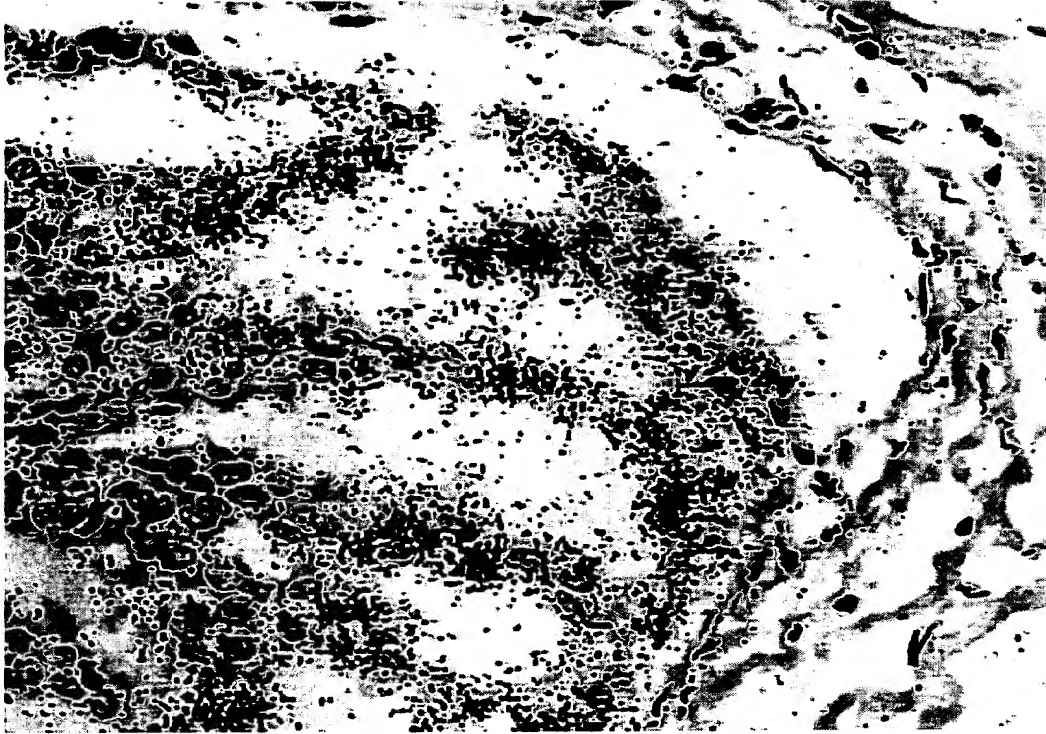


Fig. 10A



Fig. 10B